

## SEQUENCE LISTING



<110> Chiorini, John  
Kotin, Robert M.  
Safer, Brian

<120> AAV5 VECTOR AND USES THEREOF

<130> 14014.0323U3

<140> 09/717,789

<141> 2000-11-21

<150> PCT/US99/11958

<151> 1999-05-28

<150> 60/087,029

<151> 1998-05-28

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4652

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 1

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tgtcataatg	atgtaatgct	tattgtcacg	cgatagttaa	tgattaacag	tcattgtgatg	240
tgttttatcc	aataggaaga	aagcgcgcgt	atgagttctc	gcgagacttc	cggggtataa	300
aagaccgagt	gaacgagccc	gccgccattc	tttgcctcgg	actgctagag	gaccctcgct	360
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cctggaattt	ctgacagctt	tgtggactgg	gtaactggtc	aaatttgagg	gctgcctcca	480
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&lt;210&gt; 2

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 2

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Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1              5              10              15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
      20              25              30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
      35              40              45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
 50              55              60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65              70              75              80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
      85              90              95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
      100              105              110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115              120              125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130              135              140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145              150              155              160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165              170              175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
      180              185              190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
195              200              205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
210              215              220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225              230              235              240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
      245              250              255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
260              265              270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
275              280              285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
290              295              300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305              310              315              320
Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
      325              330              335
Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
340              345              350
Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
355              360              365
Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
370              375              380
Asp Ala Asn Lys Glu Gln
385              390

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&lt;210&gt; 3

&lt;211&gt; 610

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 3

Met	Ala	Thr	Phe	Tyr	Glu	Val	Ile	Val	Arg	Val	Pro	Phe	Asp	Val	Glu
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25					30		
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val
			35				40				45				
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
	50					55				60					
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
65				70						75				80	
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
				85				90						95	
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
			100					105					110		
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn
			115				120					125			
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val
	130					135					140				
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro
145				150						155				160	
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala
				165					170					175	
Leu	Asn	Leu	Glu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu
			180					185					190		
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala
		195				200						205			
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val
	210					215					220				
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
225				230						235				240	
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
				245					250					255	
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
			260					265					270		
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
		275					280					285			
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
		290				295					300				
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
305				310						315				320	
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
				325					330					335	
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
			340					345					350		
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
		355					360					365			
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
	370					375					380				
Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
385				390						395				400	
Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser
				405					410					415	
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
			420					425					430		
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys
		435					440					445			
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp
	450					455					460				

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe  
 465 470 475 480  
 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu  
 485 490 495  
 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu  
 500 505 510  
 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp  
 515 520 525  
 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg  
 530 535 540  
 Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn  
 545 550 555 560  
 Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile  
 565 570 575  
 Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp  
 580 585 590  
 Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys  
 595 600 605  
 Glu Gln  
 610

&lt;210&gt; 4

&lt;211&gt; 724

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
 synthetic construct

&lt;400&gt; 4

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
 1 5 10 15  
 Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
 20 25 30  
 Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly  
 35 40 45  
 Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
 50 55 60  
 Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
 65 70 75 80  
 Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
 85 90 95  
 Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn  
 100 105 110  
 Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe  
 115 120 125  
 Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile  
 130 135 140  
 Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
 145 150 155 160  
 Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
 165 170 175  
 Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
 180 185 190  
 Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
 195 200 205  
 Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
 210 215 220  
 Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro  
 225 230 235 240

Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg	Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp
				245					250					255	
Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr
			260					265					270		
Phe	Asp	Phe	Asn	Arg	Phe	His	Ser	His	Trp	Ser	Pro	Arg	Asp	Trp	Gln
		275					280					285			
Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val
	290					295				300					
Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Val	Gln	Asp	Ser	Thr
305					310					315					320
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp
				325					330					335	
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
			340					345					350		
Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr
		355					360					365			
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser
	370					375					380				
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn
385					390					395					400
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
				405					410					415	
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
			420					425					430		
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln
		435					440					445			
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
	450					455				460					
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
465					470					475					480
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
				485					490					495	
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
			500					505					510		
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
		515					520						525		
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
	530					535					540				
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
545					550					555					560
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
			565						570					575	
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
		580						585					590		
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
		595					600					605			
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
	610					615					620				
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
625					630					635					640
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
				645					650					655	
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
		660						665					670		
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
		675					680					685			
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
	690					695					700				
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
705					710					715					720
Thr	Arg	Pro	Leu												

&lt;210&gt; 5

&lt;211&gt; 588

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 5

Thr	Ala	Pro	Thr	Gly	Lys	Arg	Ile	Asp	Asp	His	Phe	Pro	Lys	Arg	Lys
1				5				10						15	
Lys	Ala	Arg	Thr	Glu	Glu	Asp	Ser	Lys	Pro	Ser	Thr	Ser	Ser	Asp	Ala
			20					25					30		
Glu	Ala	Gly	Pro	Ser	Gly	Ser	Gln	Gln	Leu	Gln	Ile	Pro	Ala	Gln	Pro
		35					40					45			
Ala	Ser	Ser	Leu	Gly	Ala	Asp	Thr	Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro
	50					55				60					
Leu	Gly	Asp	Asn	Asn	Gln	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly
65				70					75					80	
Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys
			85					90						95	
Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg
			100					105					110		
Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe
		115					120					125			
Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser
	130					135					140				
His	Trp	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly
145				150						155					160
Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys
			165					170						175	
Glu	Val	Thr	Val	Gln	Asp	Ser	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr
			180					185					190		
Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val
	195						200					205			
Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys	Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val
	210					215					220				
Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr	Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr
225				230						235					240
Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro
			245					250						255	
Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe
		260					265						270		
Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe
	275						280					285			
Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser
	290					295					300				
Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg
305				310					315						320
Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr
			325					330						335	
Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala
		340					345						350		
Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val
	355						360					365			
Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr
	370				375						380				
Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro
385					390					395					400

Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser Glu  
 405 410 415  
 Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly Gln  
 420 425 430  
 Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly Thr  
 435 440 445  
 Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg Asp  
 450 455 460  
 Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala  
 465 470 475 480  
 His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro  
 485 490 495  
 Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr  
 500 505 510  
 Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr  
 515 520 525  
 Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser  
 530 535 540  
 Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro  
 545 550 555 560  
 Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr  
 565 570 575  
 Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 580 585

<210> 6

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 6

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
 1 5 10 15  
 Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
 20 25 30  
 Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro  
 35 40 45  
 Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp  
 50 55 60  
 Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
 65 70 75 80  
 Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln  
 85 90 95  
 Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val  
 100 105 110  
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr  
 115 120 125  
 Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp  
 130 135 140  
 Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys  
 145 150 155 160  
 Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr  
 165 170 175  
 Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser  
 180 185 190  
 Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn  
 195 200 205



Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
210						215					220				
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
225					230					235					240
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln
				245					250					255	
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
			260					265					270		
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
		275					280					285			
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
	290					295					300				
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
305					310					315					320
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
			325						330					335	
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
			340					345					350		
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
	355						360					365			
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
	370				375						380				
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
385					390					395					400
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
			405					410						415	
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
			420					425					430		
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
	435						440					445			
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
	450					455					460				
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
465					470					475					480
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
			485						490					495	
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
		500						505					510		
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
		515					520					525			
Thr	Arg	Pro	Leu												
	530														

&lt;210&gt; 7

&lt;211&gt; 2307

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 7

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ctgcgaccgc	tcaattggaa	ttcaagtaaa	taaagcgagt	agtcattgtct	tttgttgatc	120
accctccaga	ttggttggaa	gaagtgtgtg	aaggtcttcg	cgagtttttg	ggccttgaag	180
cgggcccacc	gaaacccaaa	ccaatcagc	agcatcaaga	tcaagcccgt	ggtcttgtgc	240
tgccctggtta	taactatctc	ggaccgggaa	acggtctcga	tgcaggagag	cctgtcaaca	300
gggcagacga	ggtcgcgcga	gagcacgaca	tctcgtacaa	cgagcagctt	gaggcgggag	360
acaaccccta	cctcaagtac	aaccacgcgg	acgccgagtt	tcaggagaag	ctcgcggacg	420
acacatcctt	cgggggaaac	ctcggaaagg	cagtctttca	ggccaagaaa	agggttctcg	480

aaccttttgg	cctgggtgaa	gaggggtgcta	agacggcccc	taccggaaaag	cggatagacg	540
accactttcc	aaaaagaaaag	aaggctcggga	ccgaagagga	ctccaagcct	tccacctcgt	600
cagacgccga	agctggaccc	agcggatccc	agcagctgca	aatcccagcc	caaccagcct	660
caagtttggg	agctgataca	atgtctgctg	gaggtggcgg	cccatattggg	gacaataacc	720
aaggtgccga	tggagtgggc	aatgcctcgg	gagattggca	ttgcgattcc	acgtggatgg	780
gggacagagt	cgtcaccaag	tccacccgaa	cctgggtgct	gcccagctac	aacaaccacc	840
agtaccgaga	gatcaaaaagc	ggctccgtcg	acggaagcaa	cgccaacgcc	tactttggat	900
acagcaccac	ctgggggtac	tttgacttta	accgcttcca	cagccactgg	agcccccgag	960
actggcaaaag	actcatcaac	aactactggg	gcttcagacc	cgggtccctc	agagtcaaaa	1020
tcttcaacat	tcaagtcaaa	gaggtcacgg	tgcaggactc	caccaccacc	atcgccaaca	1080
acctcacctc	caccgtccaa	gtgtttacgg	acgacgacta	ccagctgccc	tacgtcgtcg	1140
gcaacggggc	cgagggatgc	ctgccggcct	tccctccgca	ggtctttacg	ctgccgcagt	1200
acggttacgc	gacgctgaac	cgcgacaaca	cagaaaaatcc	caccgagagg	agcagcttct	1260
tctgcctaga	gtactttccc	agcaagatgc	tgagaacggg	caacaacttt	gagtttacct	1320
acaactttga	ggaggtgccc	ttccactcca	gcttcgctcc	cagtcagaac	ctgttcaagc	1380
tggccaaccc	gctgggtggac	cagtacttgt	accgcttcgt	gagcacaaat	aacactggcg	1440
gagtccagtt	caacaagaac	ctggccggga	gatacgccaa	cacctacaaa	aactgggttc	1500
cggggcccat	gggcccgaacc	cagggctgga	acctgggctc	cgggggtcaac	cgcgccagtg	1560
tcagcgcctt	cgccacgacc	aataggatgg	agctcgaggg	cgcgagttac	caggtgcccc	1620
cgcagccgaa	cggcatgacc	aacaacctcc	agggcagcaa	cacctatgcc	ctggagaaca	1680
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gcgggcagat	ggccaccaac	aaccagagct	ccaccactgc	ccccgcgacc	ggcacgtaca	1860
acctccagga	aatcgtgccc	ggcagcgtgt	ggatggagag	ggacgtgtac	ctccaaggac	1920
ccatctgggc	caagatccca	gagacggggg	cgcactttca	ccccctcccg	gccatggggc	1980
gattcggact	caaacaccca	ccgcccataga	tgctcatcaa	gaacacgcct	gtgcccgga	2040
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aggtcaccgt	ggagatggag	tgggagctca	agaaggaaaa	ctccaagagg	tggaaccag	2160
agatccagta	cacaaacaac	tacaacgacc	cccagtttgt	ggactttgcc	cgggacagca	2220
ccgggggaata	cagaaccacc	agacctatcg	gaacccgata	ccttaccoga	cccctttaac	2280
ccattcatgt	cgcataccct	caataaaa				2307

&lt;210&gt; 8

&lt;211&gt; 2264

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 8

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ctgcgaccgc	tcaattggaa	ttcaagattg	gttggaaaga	gttgggtgaag	gtcttcgcga	120
gtttttgggc	cttgaagcgg	gcccaccgaa	acaaaaaccc	aatcagcagc	atcaagatca	180
agcccgtggt	cttgtgctgc	ctggttataa	ctatctcggg	cccggaaaacg	gtctcgatcg	240
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cggaaagcgg	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	540
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cccagcccaa	ccagcctcaa	gtttggggagc	tgatacaatg	tctgcggggag	gtggcggccc	660
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cgattccacg	tggatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	780
cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
caacgcctac	tttgatatac	gcacccctcg	ggggtacttt	gactttaacc	gcttccacag	900
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gtccctcaga	gtcaaaaatct	tcaacattca	agtcaaagag	gtcacgggtg	aggactccac	1020
caccaccatc	gccaacaacc	tcacctccac	cgtccaagtg	tttacggacg	acgactacca	1080
gctgccttac	gtcgtcggca	acgggaccga	gggatgcctg	ccggccttcc	ctccgcaggt	1140

ctttacgctg	ccgcagtagc	gttacgcgac	gctgaaccgc	gacaacacag	aaaatcccac	1200
cgagaggagc	agctttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
caacttttag	tttacctaca	actttgagga	ggtgcccttc	cactccagct	tcgctcccag	1320
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cacaaataac	actggcggag	tccagttcaa	caagaacctg	gccgggagat	acgccaacac	1440
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ggtcaaccgc	gccagtgtca	gcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
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cgtggcgtag	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
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cacgcctgtg	cccggaaata	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accgggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagaggtgg	aaccagaga	tccagtacac	aaacaactac	aacgaccccc	agtttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacac	aaccaccaga	cctatcgga	cccgatacct	2220
taccgacccc	ctttaacca	ttcatgtcgc	ataccctcaa	taaa		2264

&lt;210&gt; 9

&lt;211&gt; 2264

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 9

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gtttttgggc	cttgaagcgg	gcccaccgaa	acaaaaacc	aatcagcagc	atcaagatca	180
agcccgtggt	cttgtgtcgc	ctgggtataa	ctatctcgga	cccggaaacg	gtctcgatcg	240
aggagagcct	gtcaacaggg	cagacgaggt	cgcgcgagag	cacgacatct	cgtacaacga	300
gcagcttgag	gcgggagaca	acccctacct	caagtacaac	cacgcggacg	ccgagtttca	360
ggagaagctc	gccgacgaca	catccttcgg	gggaaacctc	ggaaaggcag	tctttcaggc	420
caagaaaagg	gtttctgaac	cttttggcct	ggttgaagag	ggtgctaaga	cggcccctac	480
cggaaagcgg	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	540
caagccttcc	acctcgtag	acgcccgaagc	tggaccacgc	ggatcccagc	agctgcaaat	600
cccagcccaa	ccagcctcaa	gtttgggagc	tgatacaatg	tctgcgggag	gtggcgggcc	660
attgggcgac	aataaccaag	gtgccgatgg	agtgggcaat	gcctcgggag	attggcattg	720
cgattccacg	tggatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	780
cagctacaac	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	840
caacgcctac	tttggataca	gcacccccctg	ggggactttt	gactttaacc	gcttccacag	900
ccactggagc	ccccgagact	ggcaaagact	catcaacaac	tactggggct	tcagaccccc	960
gtccctcaga	gtcaaaatct	tcaacattca	agtcaagag	gtcacgggtg	aggactccac	1020
caccaccatc	gccaacaacc	tcacctccac	cgtccaagtg	tttacggagc	acgactacca	1080
gctgccctac	gtcgtaggca	acgggaccga	gggatgcctg	ccggccttcc	ctccgcaggt	1140
ctttacgctg	ccgcagtagc	gttacgcgac	gctgaaccgc	gacaacacag	aaaatcccac	1200
cgagaggagc	agctttcttct	gcctagagta	ctttcccagc	aagatgctga	gaacgggcaa	1260
caacttttag	tttacctaca	actttgagga	ggtgcccttc	cactccagct	tcgctcccag	1320
tcagaacctg	ttcaagctgg	ccaacccgct	ggtggaccag	tacttgtagc	gcttcgtgag	1380
cacaaataac	actggcggag	tccagttcaa	caagaacctg	gccgggagat	acgccaacac	1440
ctacaaaaac	tggttcccgg	ggcccatggg	ccgaacccag	ggctggaacc	tgggctccgg	1500
ggtcaaccgc	gccagtgtca	gcgccttcgc	cacgaccaat	aggatggagc	tcgagggcgc	1560
gagttaccag	gtgccccgcg	agccgaacgg	catgaccaac	aacctccagg	gcagcaaacac	1620
ctatgccctg	gagaacacta	tgatcttcaa	cagccagccg	gcgaacccgg	gcaccaccgc	1680
cacgtacctc	gagggcaaca	tgctcatcac	cagcgagagc	gagacgcagc	cggatgaaccg	1740
cgtggcgtag	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	1800
cgcgaccggc	acgtacaacc	tccaggaaat	cgtgcccgcc	agcgtgtgga	tggagaggga	1860

cgtgtacctc	caaggaccca	tctgggcca	gatcccgag	acgggggccc	actttcaccc	1920
ctctccggcc	atgggcgat	tcggactcaa	acacccaccg	cccatgatgc	tcatacaaga	1980
cacgcctgtg	cccggaaata	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	2040
ccagtacagc	accgggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	2100
caagaggtgg	aaccagaga	tccagtacac	aaacaactac	aacgaccccc	agtttgtgga	2160
ctttgccccg	gacagcaccg	gggaatacag	aaccaccaga	cctatcggaa	cccgatacct	2220
tacccgaccc	ctttaaccca	ttcatgtcgc	ataccctcaa	taaa		2264

&lt;210&gt; 10

&lt;211&gt; 1292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 10

agcgcaaacg	gctcgtcgcg	cagtttctgg	cagaatcctc	gcagcgctcg	caggaggcgg	60
cttcgcagcg	tgagttctcg	gctgaccggg	tcatacaaaag	caagacttcc	cagaaatata	120
tggcgctcgt	caactggctc	gtggagcacg	gcatcacttc	cgagaagcag	tggatccagg	180
aaaatcagga	gagctacctc	tccttcaact	ccaccggcaa	ctctcggagc	cagatcaagg	240
ccgcgctcga	caacgcgacc	aaaattatga	gtctgacaaa	aagcgcggtg	gactacctcg	300
tggggagctc	cgttcccgag	gacatttcaa	aaaacagaat	ctggcaaatt	tttgagatga	360
atggctacga	cccggcctac	gcgggatcca	tcctctacgg	ctggtgtcag	cgctccttca	420
acaagaggaa	caccgtcttg	ctctacggac	ccgccacgac	cggcaagacc	aacatcgagg	480
aggccatcgc	ccacactgtg	ccctttttacg	gctgcgtgaa	ctggaccaat	gaaaactttc	540
cctttaatga	ctgtgtggac	aaaatgctca	tttggtggga	ggagggaaaag	atgaccaaca	600
aggtggttga	atccgcgaag	gccatcctgg	ggggctcaaa	ggtgcgggtc	gatcagaaat	660
gtaaatcctc	tgttcaaatt	gattctaccc	ctgtcattgt	aacttccaat	acaaacatgt	720
gtgtggtggt	ggatgggaat	tccacgacct	ttgaacacca	gcagccgctg	gaggaccgca	780
tgttcaaatt	tgaactgact	aagcggtctc	cgccagattt	tggcaagatt	actaagcagg	840
aagtcaagga	cttttttctg	tgggcaaagg	tcaatcaggt	gccgggtgact	cacgagttta	900
aagttcccg	ggaattggcg	ggaactaaag	ggcgaggaga	atctctaaaa	cgcccactgg	960
gtgacgtcac	caatactagc	tataaaagtc	tggagaagcg	ggccagggtc	tcatttgttc	1020
ccgagacgcc	tcgcagttca	gacgtgactg	ttgatcccg	tcctctgcga	ccgctcaatt	1080
ggaattcaag	gtatgattgc	aaatgtgact	atcatgtctca	atttgacaac	atttctaaca	1140
aatgtgatga	atgtgaatat	ttgaatcggg	gcaaaaatgg	atgtatctgt	cacaatgtaa	1200
ctcactgtca	aatttgtcat	gggattcccc	cctgggaaaa	ggaaaacttg	tcagattttg	1260
gggattttga	cgatgccaat	aaagaacagt	aa			1292

&lt;210&gt; 11

&lt;211&gt; 1870

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 11

attcttttct	ctggactgct	agaggaccct	cgctgccatg	gctaccttct	atgaagtcac	60
tgttcgcgct	ccatttgacg	tggaggaaca	tctgcctgga	atttctgaca	gctttgtgga	120
ctgggtaact	ggtcaaattt	gggagctgcc	tccagagtca	gattttaaatt	tgactctggg	180
tgaacagcct	cagttgacgg	tggctgatag	aattcgccgc	gtgttcctgt	acgagtggaa	240
caaatttttc	aagcaggagt	ccaaattctt	tgtgcagttt	gaaaagggat	ctgaatattt	300
tcactgcac	acgcttgtgg	agacctccgg	catctcttcc	atggtcctcg	gccgctacgt	360
gagtcagatt	cgcgcccagc	tggtgaaagt	ggtcttccag	ggaattgaac	cccagatcaa	420
cgactgggtc	gccatcacca	aggtaaagaa	ggcgaggagc	aataagggtg	tggattctgg	480
gtatattccc	gcctacctgc	tgccgaaggt	ccaaccggag	cttcagtggg	cgtggacaaa	540
cctggacgag	tataaattgg	ccgccctgaa	tctggaggag	cgcaaaccgg	tcgtcgcgca	600

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gtttctggca gaatcctcgc agcgctcgca ggaggcggtc tcgcagcgtg agttctcggc 660
tgaccgggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt 720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc 780
cttcaactcc accggcaact ctcgagacca gatcaaggcc gcgctcgaca acgcgaccaa 840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga 900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc 960
gggatccatc ctctacggct ggtgtcagcg ctcttcaaac aagaggaaca ccgtctggct 1020
ctacggaccc gccacgaccg gcaagaccaa catcgcgag gccatcgccc aactgtgcc 1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa 1140
aatgctcatt tgggtggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc 1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga 1260
ttctaccctt gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc 1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa 1380
gcggctcccc ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg 1440
ggcaaaggtc aatcagggtc cggtgactca cgagtttaaa gttcccaggg aattggcggg 1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta 1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga 1620
cgtgactggt gatccccgtc ctctgcgacc gctcaatttg aattcaagg atgattgcaa 1680
atgtgactat catgctcaat ttgacaacat ttctaacaaa tgtgatgaat gtgaatattt 1740
gaatcggggc aaaaatggat gtatctgtca caatgtaact cactgtcaaa tttgtcatgg 1800
gattccccc tgggaaaagg aaaacttgtc agattttggg gattttgacg atgccaataa 1860
agaacagtaa

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<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 12

```

Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
 1          5          10          15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
      20          25          30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
      35          40          45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
      50          55          60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
      65          70          75          80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
      85          90          95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
      100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130          135          140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
      145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
      180          185          190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
      195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
      210          215          220

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Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225          230          235          240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
          245          250          255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
          260          265          270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
          275          280          285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
          290          295          300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305          310          315          320
Trp Asn Ser Arg Leu Val Gly Arg Ser Trp
          325          330

```

&lt;210&gt; 13

&lt;211&gt; 1115

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 13

```

aggagcgcaa acggctcgtc gcgcagtttc tggcagaatc ctcgcagcgc tcgcaggagg      60
cggcttcgca gcgtgagttc tcggctgacc cggtcaccaa aagcaagact tcccagaaat      120
acatggcgct cgtcaactgg ctcgctggagc acggcatcac ttccgagaag cagtggatcc      180
aggaaaatca ggagagctac ctctccttca actccaccgg caactctcgg agccagatca      240
aggccgcgct cgacaacgcg accaaaatta tgagtctgac aaaaagcgcg gtggactacc      300
tcgtggggag ctccgttccc gaggacattt caaaaaacag aatctggcaa atttttgaga      360
tgaatggcta cgaccgggcc tacgcgggat ccatactcta cggctgggtg cagcgctcct      420
tcaacaagag gaacaccgtc tggctctacg gaccgccac gaccggcaag accaacatcg      480
cggaggccat cgccacact gtgccctttt acggctgcgt gaactggacc aatgaaaact      540
ttccctttaa tgactgtgtg gacaaaatgc tcatttggtg ggaggaggga aagatgacca      600
acaaggtggt tgaatccgcc aaggccatcc tggggggctc aaaggtgcgg gtcgatcaga      660
aatgtaaate ctctgttcaa attgattcta cccctgtcat tgtaacttcc aatacaaaca      720
tgtgtgtggt ggtggatggg aattccacga cctttgaaca ccagcagccg ctggaggacc      780
gcatgttcaa atttgaactg actaagcggc tcccgccaga ttttggcaag attactaagc      840
aggaagtcaa ggactttttt gcttgggcaa aggtcaatca ggtgccggtg actcacgagt      900
ttaaagttcc caggggaattg gcgggaacta aaggggcgga gaaatctcta aaacgcccac      960
tggtgtgacgt caccaatact agctataaaa gtctggagaa gcggggccagg ctctcatttg     1020
ttcccagac gcctcgagc ttagacgtga ctgttgatcc cgctcctctg cgaccgctca     1080
attggaattc aagattggtt ggaagaagtt ggtga                                     1115

```

&lt;210&gt; 14

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 14

```

Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
  1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
          20          25          30

```

Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Val	35	40	45
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu	50	55	60
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln	65	70	75
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr	85	90	95
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg	100	105	110
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Gly	Ile	Glu	Pro	Gln	Ile	Asn	115	120	125
Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val	130	135	140
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro	145	150	155
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Asp	Glu	Tyr	Lys	Leu	Ala	Ala	165	170	175
Leu	Asn	Leu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Leu	Ala	Glu		180	185	190
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ser	Gln	Arg	Glu	Phe	Ser	Ala		195	200	205
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val	210	215	220
Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln	225	230	235
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg	245	250	255
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu	260	265	270
Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp	275	280	285
Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp	290	295	300
Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe	305	310	315
Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys	325	330	335
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys	340	345	350
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys	355	360	365
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu	370	375	380
Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys	385	390	395
Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser	405	410	415
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu	420	425	430
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys	435	440	445
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp	450	455	460
Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe	465	470	475
Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala	Glu	Lys	Ser	Leu	485	490	495
Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr	Lys	Ser	Leu	Glu	500	505	510





<210> 17  
 <211> 174  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 17  
 taagcaggaa gtcaaggact tttttgcttg ggcaaagggtc aatcagggtgc cggtgactca 60  
 cgagttttaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg 120  
 cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag 174

<210> 18  
 <211> 187  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 18  
 cactctcaag caaggggggtt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc 60  
 acgcgatagt taatgattaa cagtcattgt atgtgtttta tccaatagga agaaagcgcg 120  
 cgtatgagtt ctgcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca 180  
 ttctttg 187

<210> 19  
 <211> 168  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 19  
 aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc 60  
 tcgtttgggg ggggtggcagc tcaaagagct gccagacgac ggccctctgg ccgtcgcccc 120  
 cccaaacgag ccagcgagcg agcgaacgag acagggggga gagtgcc 168

<210> 20  
 <211> 168  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 20  
 aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc 60  
 tcgtttgggg gggcgacggc cagagggccg tcgtctgccg gctctttgag ctgccacccc 120  
 cccaaacgag ccagcgagcg agcgaacgag acagggggga gagtgcc 168

<210> 21  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 21

cggtgtga

8

<210> 22

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 22

cggttgag

8

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 23

caaaacctcc ttgcttgaga g

21

<210> 24

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 24

Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Thr	Leu	Ser
1				5					10					15	
Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
		20						25				30			
Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro	
		35				40					45				
Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50				55				60						
Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65			70						75					80	
Arg	Gln	Leu	Asp	Ser	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
			85				90						95		
Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
		100					105						110		
Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
		115				120					125				
Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
	130					135					140				

Pro Val Glu His Ser	Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly	145	150	155	160
Lys Ala Gly Gln Gln	Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr	165	170	175	
Gly Asp Ala Asp Ser	Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro	180	185	190	
Ala Ala Pro Ser Gly	Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly	195	200	205	
Ala Pro Met Ala Asp	Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser	210	215	220	
Ser Gly Asn Trp His	Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile	225	230	235	240
Thr Thr Ser Thr Arg	Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu	245	250	255	
Tyr Lys Gln Ile Ser	Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr	260	265	270	
Phe Gly Tyr Ser Thr	Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His	275	280	285	
Cys His Phe Ser Pro	Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp	290	295	300	
Gly Phe Arg Pro Lys	Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val	305	310	315	320
Lys Glu Val Thr Gln	Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu	325	330	335	
Thr Ser Thr Val Gln	Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr	340	345	350	
Val Leu Gly Ser Ala	His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp	355	360	365	
Val Phe Met Val Pro	Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser	370	375	380	
Gln Ala Val Gly Arg	Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser	385	390	395	400
Gln Met Leu Arg Thr	Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu	405	410	415	
Asp Val Pro Phe His	Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg	420	425	430	
Leu Met Asn Pro Leu	Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr	435	440	445	
Asn Thr Pro Ser Gly	Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln	450	455	460	
Ala Gly Ala Ser Asp	Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly	465	470	475	480
Pro Cys Tyr Arg Gln	Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn	485	490	495	
Asn Ser Glu Tyr Ser	Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly	500	505	510	
Arg Asp Ser Leu Val	Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp	515	520	525	
Asp Glu Glu Lys Phe	Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys	530	535	540	
Gln Gly Ser Glu Lys	Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr	545	550	555	560
Asp Glu Glu Glu Ile	Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr	565	570	575	
Gly Ser Val Ser Thr	Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr	580	585	590	
Ala Asp Val Asn Thr	Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp	595	600	605	
Arg Asp Val Tyr Leu	Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr	610	615	620	

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Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                      630                      635                      640
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                      645                      650                      655
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
                      660                      665                      670
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
                      675                      680                      685
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
                      690                      695                      700
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                      710                      715                      720
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                      725                      730                      735

```

&lt;210&gt; 25

&lt;211&gt; 4679

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 25

```

ttggccactc cctctctgcg cgctcgctcg ctactgagg cggggcgacc aaaggtcgcc      60
cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg      120
gccaactcca tcactagggg ttcttgagg ggtggagtcg tgacgtgaat tacgtcatag      180
ggttaggagg gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacacccat      240
gtggtcacgc tgggtattta agcccagtg agcacgcagg gtctccattt tgaagcggga      300
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accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg      420
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&lt;210&gt; 26

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 26

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Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1             5             10             15
Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
             20             25             30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
             35             40             45

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Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
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Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
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Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
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Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
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Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
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Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
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Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
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Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
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Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
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Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
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Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
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Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
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Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
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Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
			515					520					525		

Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
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Phe	Pro	Val	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
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Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
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Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
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